

# SEQUENCE LISTING

<110> Japan Science and Technology Corporation

<120> Amino Acid Transporter And Gene Thereof

<130> PC901338

<140>

<141>

<160> 27

<210> 1

<211> 4539

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> (1)..(65)

<220>

<221> CDS

<222> (66)..(1589)

<220>

<221> 3'UTR

<222> (1590)..(4474)

<400> 1

cggcgcgcac actgctcgct gggccgcggc tcccgggtgt cccaggcccg gccggtgcgc 60

agagc atg gcg ggt gcg ggc ccg aag cgg cgc gcg cta gcg gcg ccg gcg 110  
Met Ala Gly Ala Gly Pro Lys Arg Arg Ala Leu Ala Ala Pro Ala  
1 5 10 15

gcc gag gag aag gaa gag gcg cgg gag aag atg ctg gcc gcc aag agc 158  
Ala Glu Glu Lys Glu Glu Ala Arg Glu Lys Met Leu Ala Ala Lys Ser  
20 25 30

gcg gac ggc tcg gcg ccg gca ggc gag ggc gag ggc gtg acc ctg cag 206  
Ala Asp Gly Ser Ala Pro Ala Gly Glu Gly Glu Gly Val Thr Leu Gln  
35 40 45

cgg aac atc acg ctg ctc aac ggc gtg gcc atc atc gtg ggg acc att 254  
Arg Asn Ile Thr Leu Leu Asn Gly Val Ala Ile Ile Val Gly Thr Ile  
50 55 60

atc ggc tcg ggc atc ttc gtg acg ccc acg ggc gtg ctc aag gag gca 302  
Ile Gly Ser Gly Ile Phe Val Thr Pro Thr Gly Val Leu Lys Glu Ala  
65 70 75

ggc tcg ccg ggg ctg gcg ctg gtg gtg tgg gcc gcg tgc ggc gtc ttc 350  
Gly Ser Pro Gly Leu Ala Leu Val Val Trp Ala Ala Cys Gly Val Phe



80	85	90	95	
tcc atc gtg ggc gcg ctc tgc tac gcg gag ctc ggc acc acc atc tcc				398
Ser Ile Val Gly Ala Leu Cys Tyr Ala Glu Leu Gly Thr Thr Ile Ser	100	105	110	
aaa tcg ggc ggc gac tac gcc tac atg ctg gag gtc tac ggc tcg ctg				446
Lys Ser Gly Gly Asp Tyr Ala Tyr Met Leu Glu Val Tyr Gly Ser Leu	115	120	125	
ccc gcc ttc ctc aag ctc tgg atc gag ctg ctc atc atc cgg cct tca				494
Pro Ala Phe Leu Lys Leu Trp Ile Glu Leu Leu Ile Ile Arg Pro Ser	130	135	140	
tcg cag tac atc gtg gcc ctg gtc ttc gcc acc tac ctg ctc aag ccg				542
Ser Gln Tyr Ile Val Ala Leu Val Phe Ala Thr Tyr Leu Leu Lys Pro	145	150	155	
ctc ttc ccc acc tgc ccg gtg ccc gag gag gca gcc aag ctc gtg gcc				590
Leu Phe Pro Thr Cys Pro Val Pro Glu Glu Ala Ala Lys Leu Val Ala	160	165	170	175
tgc ctc tgc gtg ctg ctg ctc acg gcc gtg aac tgc tac agc gtg aag				638
Cys Leu Cys Val Leu Leu Leu Thr Ala Val Asn Cys Tyr Ser Val Lys	180	185	190	
gcc gcc acc cgg gtc cag gat gcc ttt gcc gcc gcc aag ctc ctg gcc				686
Ala Ala Thr Arg Val Gln Asp Ala Phe Ala Ala Ala Lys Leu Leu Ala	195	200	205	
ctg gcc ctg atc atc ctg ctg ggc ttc gtc cag atc ggg aag ggt gat				734
Leu Ala Leu Ile Ile Leu Leu Gly Phe Val Gln Ile Gly Lys Gly Asp	210	215	220	
gtg tcc aat cta gat ccc aac ttc tca ttt gaa ggc acc aaa ctg gat				782
Val Ser Asn Leu Asp Pro Asn Phe Ser Phe Glu Gly Thr Lys Leu Asp	225	230	235	
gtg ggg aac att gtg ctg gca tta tac agc ggc ctc ttt gcc tat gga				830
Val Gly Asn Ile Val Leu Ala Leu Tyr Ser Gly Leu Phe Ala Tyr Gly	240	245	250	255
gga tgg aat tac ttg aat ttc gtc aca gag gaa atg atc aac ccc tac				878
Gly Trp Asn Tyr Leu Asn Phe Val Thr Glu Glu Met Ile Asn Pro Tyr	260	265	270	
aga aac ctg ccc ctg gcc atc atc atc tcc ctg ccc atc gtg acg ctg				926
Arg Asn Leu Pro Leu Ala Ile Ile Ile Ser Leu Pro Ile Val Thr Leu	275	280	285	
gtg tac gtg ctg acc aac ctg gcc tac ttc acc acc ctg tcc acc gag				974
Val Tyr Val Leu Thr Asn Leu Ala Tyr Phe Thr Thr Leu Ser Thr Glu	290	295	300	
cag atg ctg tcg tcc gag gcc gtg gcc gtg gac ttc ggg aac tat cac				1022
Gln Met Leu Ser Ser Glu Ala Val Ala Val Asp Phe Gly Asn Tyr His	305	310	315	

ctg ggc gtc atg tcc tgg atc atc ccc gtc ttc gtg ggc ctg tcc tgc	1070
Leu Gly Val Met Ser Trp Ile Ile Pro Val Phe Val Gly Leu Ser Cys	
320 325 330 335	
ttc ggc tcc gtc aat ggg tcc ctg ttc aca tcc tcc agg ctc ttc ttc	1118
Phe Gly Ser Val Asn Gly Ser Leu Phe Thr Ser Ser Arg Leu Phe Phe	
340 345 350	
gtg ggg tcc cgg gaa ggc cac ctg ccc tcc atc ctc tcc atg atc cac	1166
Val Gly Ser Arg Glu Gly His Leu Pro Ser Ile Leu Ser Met Ile His	
355 360 365	
cca cag ctc ctc acc ccc gtg ccg tcc ctc gtg ttc acg tgt gtg atg	1214
Pro Gln Leu Leu Thr Pro Val Pro Ser Leu Val Phe Thr Cys Val Met	
370 375 380	
acg ctg ctc tac gcc ttc tcc aag gac atc ttc tcc gtc atc aac ttc	1262
Thr Leu Leu Tyr Ala Phe Ser Lys Asp Ile Phe Ser Val Ile Asn Phe	
385 390 395	
ttc agc ttc ttc aac tgg ctc tgc gtg gcc ctg gcc atc atc ggc atg	1310
Phe Ser Phe Phe Asn Trp Leu Cys Val Ala Leu Ala Ile Ile Gly Met	
400 405 410 415	
atc tgg ctg cgc cac aga aag cct gag ctt gag cgg ccc atc aag gtg	1358
Ile Trp Leu Arg His Arg Lys Pro Glu Leu Glu Arg Pro Ile Lys Val	
420 425 430	
aac ctg gcc ctg cct gtg ttc ttc atc ctg gcc tgc ctc ttc ctg atc	1406
Asn Leu Ala Leu Pro Val Phe Phe Ile Leu Ala Cys Leu Phe Leu Ile	
435 440 445	
gcc gtc tcc ttc tgg aag aca ccc gtg gag tgt ggc atc ggc ttc acc	1454
Ala Val Ser Phe Trp Lys Thr Pro Val Glu Cys Gly Ile Gly Phe Thr	
450 455 460	
atc atc ctc agc ggg ctg ccc gtc tac ttc ttc ggg gtc tgg tgg aaa	1502
Ile Ile Leu Ser Gly Leu Pro Val Tyr Phe Phe Gly Val Trp Trp Lys	
465 470 475	
aac aag ccc aag tgg ctc ctc cag ggc atc ttc tcc acg acc gtc ctg	1550
Asn Lys Pro Lys Trp Leu Leu Gln Gly Ile Phe Ser Thr Thr Val Leu	
480 485 490 495	
tgt cag aag ctc atg cag gtg gtc ccc cag gag aca tag ccaggaggcc	1599
Cys Gln Lys Leu Met Gln Val Val Pro Gln Glu Thr	
500 505	
gagtggtctgc cggaggagca tgcgcagagg ccagttaaag tagatcacct cctcgaaccc 1659	
actccggttc cccgcaaccc acagctcagc tgcccatccc agtccctcgc cgtccctccc 1719	
aggtcggggca gtggaggctg ctgtgaaaac tctggtacga atctcatccc tcaactgagg 1779	
gccaggggacc caggtgtgcc tgtgctcctg cccaggagca gcttttggtc tccttggggc 1839	

ctttttccct tccctccttt gtttacttat atatatattt tttttaaact taaatttttg 1899  
gtcaacttga caccactaag atgatttttt aaggagctgg gggaaggcag gagccttcct 1959  
ttctcctgcc ccaagggccc agaccctggg caaacagagc tactgagact tggaacctca 2019  
ttgctacgac agacttgac tgaagccgga cagctgcca gacacatggg cttgtgacat 2079  
tcgtgaaaac caaccctgtg ggcttatgtc tctgccttag ggtttgaga gtggaaactc 2139  
agccgtaggg tggcactggg aggggggtgg ggatctgggc aagggtgggtg attcctccca 2199  
ggaggtgctt gaggccccga tggactcctg accataatcc tagccccgag acaccatcct 2259  
gagccagga acagccccag ggttgggggg tgccggcatc tcccctagct caccaggcct 2319  
ggcctctggg cagtgtggcc tcttggctat ttctgttcca gttttggagg ctgagttctg 2379  
gttcatgcag acaaagccct gtccttcagt cttctagaaa cagagacaag aaaggcagac 2439  
acaccgcggc caggcaccca tgtgggcgcc caccctgggc tccacacagc agtgtcccct 2499  
gccccagagg tcgcagctac cctcagcctc caatgcattg gcctctgtac cgccccgag 2559  
ccccttctgg ccggtgctgg gttcccactc ccggcctagg cacctccccg ctctccctgt 2619  
cacgctcatg tcctgtcctg gtcctgatgc ccgttgtcta ggagacagag ccaagcactg 2679  
ctcacgtctc tgccgcctgc gtttggaggc ccctgggctc tcaccagtc cccaccgcc 2739  
tgagagagg gaactagggc accccttggt tctgttggtc ccgtgaattt ttttcgctat 2799  
gggaggcagc cgaggcctgg ccaatgcggc ccactttcct gagctgtcgc tgcctccatg 2859  
gcagcagcca aggaccccca gaacaagaag accccccgc aggatccctc ctgagctcgg 2919  
ggggctctgc cttctcaggc cccgggcttc ctttctcccc agccagaggt ggagccaagt 2979  
ggtccagcgt cactccagtg ctcagctgtg gctggaggag ctggcctgtg gcacagccct 3039  
gagtgtccca agccgggagc caacgaagcc ggacacggct tactgacca gcggctgctc 3099  
aagccgcaag ctctcagcaa gtgcccagtg gagcctgccg cccccacctg ggcaccggga 3159  
ccccctcacc atccagtggg cccggagaaa cctgatgaac agtttgggga ctcaggacca 3219  
gatgtccgtc tctcttgctt gaggaatgaa gaccttatt caccctgcc ccgttgcttc 3279  
ccgctgcaca tggacagact tcacagcgtc tgctcatagg acctgcatcc ttctgggga 3339  
cgaattccac tcgtccaagg gacagcccac ggtctggagg ccgaggacca ccagcaggca 3399  
ggtggactga ctgtgttggg caagacctct tccctctggg cctgttctct tggctgaaa 3459  
taaggacagc agctggtgcc ccacctgcct ggtgcattgc tgtgtgaatc caggaggcag 3519  
tggacatcgt aggcagccac ggccccgggt ccaggagaag tgctccctgg aggcacgcac 3579

cactgcttcc cactggggcc ggcgggggccc acgcacgacg tcagcctctt accttcccgc 3639  
 ctcggtctagg ggtcctcggg atgccgttct gttccaacct cctgctctgg gaggtggaca 3699  
 tgcctcaagg atacagggag ccggcggcct ctcgacggca cgcacttgcc tgttggtgc 3759  
 tgcggtctgtg ggcgagcatg ggggctgcc a gcgtctgttg tggaaagtag ctgctagtga 3819  
 aatggctggg gccgctgggg tccgtcttca cactgcgag gtctcttctg ggcgtctgag 3879  
 ctgggggtggg agctcctccg cagaaggttg gtgggggggc cagtctgtga tccttggtgc 3939  
 tgtgtgcccc actccagcct ggggacccca cttcagaagg taggggccgt gtcccgcggt 3999  
 gctgactgag gcctgcttcc ccctccccct cctgctgtgc tgggaattcca cagggaccag 4059  
 gggcaccgca ggggactgtc tcagaagact tgatttttcc gtcccttttt ctccacactc 4119  
 cactgacaaa cgtccccagc ggtttccact tgtgggcttc aggtgttttc aagcacaacc 4179  
 caccacaaca agcaagtgc ttttcagtcg ttgtgctttt ttgttttgtg ctaacgtctt 4239  
 actaatttaa agatgctgtc ggcaccatgt ttattttatt ccagtggta tgctcagcct 4299  
 tgctgctctg cgtggcgag gtgccatgcc tgctccctgt ctgtgtccca gccacgcagg 4359  
 gccatccact gtgacgtcgg ccgaccaggc tggacaccct ctgccgagta atgacgtgtg 4419  
 tggctgggac cttctttatt ctgtgttaat ggctaacctg ttacactggg ctgggttggg 4479  
 taggggtgtc tggctttttt gtgggggttt tatttttaaa gaaacactca atcatcctag 4539

<210> 2

<211> 507

<212> PRT

<213> Homo sapiens

<400> 2

Met	Ala	Gly	Ala	Gly	Pro	Lys	Arg	Arg	Ala	Leu	Ala	Ala	Pro	Ala	Ala
1				5					10					15	
Glu	Glu	Lys	Glu	Glu	Ala	Arg	Glu	Lys	Met	Leu	Ala	Ala	Lys	Ser	Ala
			20					25					30		
Asp	Gly	Ser	Ala	Pro	Ala	Gly	Glu	Gly	Glu	Gly	Val	Thr	Leu	Gln	Arg
		35					40					45			
Asn	Ile	Thr	Leu	Leu	Asn	Gly	Val	Ala	Ile	Ile	Val	Gly	Thr	Ile	Ile
	50					55					60				
Gly	Ser	Gly	Ile	Phe	Val	Thr	Pro	Thr	Gly	Val	Leu	Lys	Glu	Ala	Gly
	65				70					75					80
Ser	Pro	Gly	Leu	Ala	Leu	Val	Val	Trp	Ala	Ala	Cys	Gly	Val	Phe	Ser
			85						90					95	

Ile	Val	Gly	Ala	Leu	Cys	Tyr	Ala	Glu	Leu	Gly	Thr	Thr	Ile	Ser	Lys	100	105	110
Ser	Gly	Gly	Asp	Tyr	Ala	Tyr	Met	Leu	Glu	Val	Tyr	Gly	Ser	Leu	Pro	115	120	125
Ala	Phe	Leu	Lys	Leu	Trp	Ile	Glu	Leu	Leu	Ile	Ile	Arg	Pro	Ser	Ser	130	135	140
Gln	Tyr	Ile	Val	Ala	Leu	Val	Phe	Ala	Thr	Tyr	Leu	Leu	Lys	Pro	Leu	145	150	155
Phe	Pro	Thr	Cys	Pro	Val	Pro	Glu	Glu	Ala	Ala	Lys	Leu	Val	Ala	Cys	165	170	175
Leu	Cys	Val	Leu	Leu	Leu	Thr	Ala	Val	Asn	Cys	Tyr	Ser	Val	Lys	Ala	180	185	190
Ala	Thr	Arg	Val	Gln	Asp	Ala	Phe	Ala	Ala	Ala	Lys	Leu	Leu	Ala	Leu	195	200	205
Ala	Leu	Ile	Ile	Leu	Leu	Gly	Phe	Val	Gln	Ile	Gly	Lys	Gly	Asp	Val	210	215	220
Ser	Asn	Leu	Asp	Pro	Asn	Phe	Ser	Phe	Glu	Gly	Thr	Lys	Leu	Asp	Val	225	230	235
Gly	Asn	Ile	Val	Leu	Ala	Leu	Tyr	Ser	Gly	Leu	Phe	Ala	Tyr	Gly	Gly	245	250	255
Trp	Asn	Tyr	Leu	Asn	Phe	Val	Thr	Glu	Glu	Met	Ile	Asn	Pro	Tyr	Arg	260	265	270
Asn	Leu	Pro	Leu	Ala	Ile	Ile	Ile	Ser	Leu	Pro	Ile	Val	Thr	Leu	Val	275	280	285
Tyr	Val	Leu	Thr	Asn	Leu	Ala	Tyr	Phe	Thr	Thr	Leu	Ser	Thr	Glu	Gln	290	295	300
Met	Leu	Ser	Ser	Glu	Ala	Val	Ala	Val	Asp	Phe	Gly	Asn	Tyr	His	Leu	305	310	315
Gly	Val	Met	Ser	Trp	Ile	Ile	Pro	Val	Phe	Val	Gly	Leu	Ser	Cys	Phe	325	330	335
Gly	Ser	Val	Asn	Gly	Ser	Leu	Phe	Thr	Ser	Ser	Arg	Leu	Phe	Phe	Val	340	345	350
Gly	Ser	Arg	Glu	Gly	His	Leu	Pro	Ser	Ile	Leu	Ser	Met	Ile	His	Pro	355	360	365
Gln	Leu	Leu	Thr	Pro	Val	Pro	Ser	Leu	Val	Phe	Thr	Cys	Val	Met	Thr	370	375	380
Leu	Leu	Tyr	Ala	Phe	Ser	Lys	Asp	Ile	Phe	Ser	Val	Ile	Asn	Phe	Phe	385	390	395

Ser Phe Phe Asn Trp Leu Cys Val Ala Leu Ala Ile Ile Gly Met Ile  
 405 410 415  
 Trp Leu Arg His Arg Lys Pro Glu Leu Glu Arg Pro Ile Lys Val Asn  
 420 425 430  
 Leu Ala Leu Pro Val Phe Phe Ile Leu Ala Cys Leu Phe Leu Ile Ala  
 435 440 445  
 Val Ser Phe Trp Lys Thr Pro Val Glu Cys Gly Ile Gly Phe Thr Ile  
 450 455 460  
 Ile Leu Ser Gly Leu Pro Val Tyr Phe Phe Gly Val Trp Trp Lys Asn  
 465 470 475 480  
 Lys Pro Lys Trp Leu Leu Gln Gly Ile Phe Ser Thr Thr Val Leu Cys  
 485 490 495  
 Gln Lys Leu Met Gln Val Val Pro Gln Glu Thr  
 500 505

<210> 3  
 <211> 3455  
 <212> DNA  
 <213> Rat

<220>  
 <221> 5'UTR  
 <222> (1)..(63)

<220>  
 <221> CDS  
 <222> (64)..(1602)

<220>  
 <221> 3'UTR  
 <222> (1603)..(3455)

<400> 3  
 cgcgagagagc ggctcggccg cgcgcacgcc gggatatccag gccgagccgg gaacgtcgag 60

agc atg gcg gtc gcg ggc gca aag cgg cgc gcg gtt gcg gcc ccc gcg 108  
 Met Ala Val Ala Gly Ala Lys Arg Arg Ala Val Ala Ala Pro Ala  
 1 5 10 15

acg acg gcg gcg gag gag gag cgg cag gcg cgg gag aag atg ctg gag 156  
 Thr Thr Ala Ala Glu Glu Glu Arg Gln Ala Arg Glu Lys Met Leu Glu  
 20 25 30

gcg cgg cgc ggg gac ggc gcg gac ccc gag ggc gaa ggc gtg acc ctg 204  
 Ala Arg Arg Gly Asp Gly Ala Asp Pro Glu Gly Glu Gly Val Thr Leu  
 35 40 45

cag cgc aat atc aca ctg atc aat ggt gtg gcc atc ata gtg ggc acc 252  
 Gln Arg Asn Ile Thr Leu Ile Asn Gly Val Ala Ile Ile Val Gly Thr

50					55					60						
atc	atc	ggt	tcg	ggc	atc	ttc	gtg	acg	ccc	acc	ggc	gtg	ctc	aag	gaa	300
Ile	Ile	Gly	Ser	Gly	Ile	Phe	Val	Thr	Pro	Thr	Gly	Val	Leu	Lys	Glu	
65					70					75						
gcc	ggc	tcg	ccc	gga	ctg	tcg	ctt	gtg	gtg	tgg	gct	gtg	tgc	ggc	gtc	348
Ala	Gly	Ser	Pro	Gly	Leu	Ser	Leu	Val	Val	Trp	Ala	Val	Cys	Gly	Val	
80					85					90					95	
ttc	tcc	atc	gtg	ggc	gca	ctg	tgc	tac	gcg	gag	ctg	ggc	act	acc	atc	396
Phe	Ser	Ile	Val	Gly	Ala	Leu	Cys	Tyr	Ala	Glu	Leu	Gly	Thr	Thr	Ile	
100					105					110						
tca	aag	tca	ggc	ggc	gac	tat	gcc	tac	atg	cta	gag	gtc	tac	ggc	tcg	444
Ser	Lys	Ser	Gly	Gly	Asp	Tyr	Ala	Tyr	Met	Leu	Glu	Val	Tyr	Gly	Ser	
115					120					125						
ctg	ccc	gcc	ttc	ctc	aag	ctc	tgg	atc	gag	ctg	ctc	atc	att	cgg	ccc	492
Leu	Pro	Ala	Phe	Leu	Lys	Leu	Trp	Ile	Glu	Leu	Leu	Ile	Ile	Arg	Pro	
130					135					140						
tcc	tca	cag	tac	atc	gtg	gcg	ctg	gtc	ttc	gcc	aca	tac	ctg	ctc	aag	540
Ser	Ser	Gln	Tyr	Ile	Val	Ala	Leu	Val	Phe	Ala	Thr	Tyr	Leu	Leu	Lys	
145					150					155						
ccg	gtc	ttc	ccc	act	tgt	ccc	gtg	ccc	gag	gag	gct	gcc	aag	ctc	gtg	588
Pro	Val	Phe	Pro	Thr	Cys	Pro	Val	Pro	Glu	Glu	Ala	Ala	Lys	Leu	Val	
160					165					170					175	
gcc	tgc	ctc	tgc	gtg	cta	cta	ctc	acg	gct	gtg	aac	tgc	tac	agt	gtg	636
Ala	Cys	Leu	Cys	Val	Leu	Leu	Leu	Thr	Ala	Val	Asn	Cys	Tyr	Ser	Val	
180					185					190						
aag	gct	gct	acc	cgt	gtg	cag	gat	gcc	ttt	gcg	gct	gcc	aaa	ctg	ctg	684
Lys	Ala	Ala	Thr	Arg	Val	Gln	Asp	Ala	Phe	Ala	Ala	Ala	Lys	Leu	Leu	
195					200					205						
gcc	ctg	gcc	ctc	atc	atc	ctg	ctc	ggc	ttc	atc	cag	atg	gga	aag	gac	732
Ala	Leu	Ala	Leu	Ile	Ile	Leu	Leu	Gly	Phe	Ile	Gln	Met	Gly	Lys	Asp	
210					215					220						
ata	gga	caa	ggg	gat	gca	tcc	aac	ctg	cac	cag	aag	ttg	tcc	ttt	gaa	780
Ile	Gly	Gln	Gly	Asp	Ala	Ser	Asn	Leu	His	Gln	Lys	Leu	Ser	Phe	Glu	
225					230					235						
ggc	acc	aat	ctg	gac	gtg	ggg	aac	att	gtg	ttg	gca	ttg	tac	agt	ggc	828
Gly	Thr	Asn	Leu	Asp	Val	Gly	Asn	Ile	Val	Leu	Ala	Leu	Tyr	Ser	Gly	
240					245					250					255	
ctc	ttc	gcc	tac	gga	gga	tgg	aac	tat	ctg	aat	ttt	gtc	acg	gag	gag	876
Leu	Phe	Ala	Tyr	Gly	Gly	Trp	Asn	Tyr	Leu	Asn	Phe	Val	Thr	Glu	Glu	
260					265					270						
atg	atc	aac	ccc	tac	agg	aac	ctc	ccc	ctg	gcc	atc	atc	atc	tcc	ttg	924
Met	Ile	Asn	Pro	Tyr	Arg	Asn	Leu	Pro	Leu	Ala	Ile	Ile	Ile	Ser	Leu	
275					280					285						



ccc att gtc acc ctg gtc tat gtg ctg acg aac ctg gcc tac ttc act	972
Pro Ile Val Thr Leu Val Tyr Val Leu Thr Asn Leu Ala Tyr Phe Thr	
290 295 300	
acc ctg tct acc aac cag atg ctg aca tct gaa gcc gtg gct gtg gat	1020
Thr Leu Ser Thr Asn Gln Met Leu Thr Ser Glu Ala Val Ala Val Asp	
305 310 315	
ttt ggg aac tac cac ctg gga gtc atg tcc tgg atc att cct gtc ttc	1068
Phe Gly Asn Tyr His Leu Gly Val Met Ser Trp Ile Ile Pro Val Phe	
320 325 330 335	
gtg ggc ttg tcc tgc ttc ggc tct gtc aat ggg tct ctg ttc acg tcc	1116
Val Gly Leu Ser Cys Phe Gly Ser Val Asn Gly Ser Leu Phe Thr Ser	
340 345 350	
tca aga ctg ttc ttc gtg gga tcc agg gag ggc cac ctg cct tcc atc	1164
Ser Arg Leu Phe Phe Val Gly Ser Arg Glu Gly His Leu Pro Ser Ile	
355 360 365	
ctc tcc atg atc cac cca cag ctt ctg aca ccg gtg cca tca ctg gtg	1212
Leu Ser Met Ile His Pro Gln Leu Leu Thr Pro Val Pro Ser Leu Val	
370 375 380	
ttc acg tgt gtc atg acc ctg atg tac gcc ttc tcc aga gac atc ttc	1260
Phe Thr Cys Val Met Thr Leu Met Tyr Ala Phe Ser Arg Asp Ile Phe	
385 390 395	
tcc atc atc aac ttc ttc agc ttc ttc aac tgg ctg tgt gtg gcc ctg	1308
Ser Ile Ile Asn Phe Phe Ser Phe Phe Asn Trp Leu Cys Val Ala Leu	
400 405 410 415	
gcc atc atc ggc atg atg tgg ctc cgc ttt aag aag cct gag ctg gag	1356
Ala Ile Ile Gly Met Met Trp Leu Arg Phe Lys Lys Pro Glu Leu Glu	
420 425 430	
cgt ccc atc aag gtg aat ctg gcc ctc cca gtg ttc ttt atc ctg gcc	1404
Arg Pro Ile Lys Val Asn Leu Ala Leu Pro Val Phe Phe Ile Leu Ala	
435 440 445	
tgc ctc ttc ctc atc gcc gtg tcc ttc tgg aag aca ccc ctg gag tgc	1452
Cys Leu Phe Leu Ile Ala Val Ser Phe Trp Lys Thr Pro Leu Glu Cys	
450 455 460	
ggc att ggc ttc gcc atc atc ctc agc ggg ctg cct gtc tac ttc ttt	1500
Gly Ile Gly Phe Ala Ile Ile Leu Ser Gly Leu Pro Val Tyr Phe Phe	
465 470 475	
ggt gtg tgg tgg aaa aac aag ccc aaa tgg atc ctg cag gtc atc ttc	1548
Gly Val Trp Trp Lys Asn Lys Pro Lys Trp Ile Leu Gln Val Ile Phe	
480 485 490 495	
tcc gtg acc gtg ctc tgc cag aag ctg atg cag gtg gtt cct cag gag	1596
Ser Val Thr Val Leu Cys Gln Lys Leu Met Gln Val Val Pro Gln Glu	
500 505 510	

act tag ccacgtgtcc tgggtgccgc gggagagtgc actgtgactg cttccagaca 1652  
 Thr  
 actcaccttt ggaaaagcag cgtccaggcc cgtcatcccc acagctccag tgagcaccac 1712  
 taactatctt aacaccatcc gctgtccctc aaaggtcagg tgtccacagt ggccgtgaaa 1772  
 gaaacctggt acgaatttgg tcccagatgg tgaccatcca tgcatacata gcagccactg 1832  
 tgagggtgtgc tgtggcctga ggccctggtct ttctgacttt ggggactgcc acatctgggc 1892  
 tttctcctct atgatttttt gttttgtttt tgtagcgttc atttgggtca agtttacact 1952  
 accgagatga ttattttttt acaaaacagg gtagcaaaga gcaggagatg gtgtggcccg 2012  
 acagtccggc tctgagtggg aactgcaggc cacagctctt ctccgactgt tgttcgttca 2072  
 gtagcacatt gtggctggag gggaccacat cactgtcacc aagtcagaac tactgagact 2132  
 caaacatcac cttttccact gtggacttgc actgacaaac ggacgatgaa tgtgctagct 2192  
 tgggtttgag ttttctgggt ctgtcctaga gatgaaaccc caacctgacc cacgaggcag 2252  
 agctctactg tgggtcattt gttccattgt aaatgcagag ctccggtctg accactctga 2312  
 agtcctggtg attccccttc ccctggctcc aaatgaaaga cctctgcagc cataacccta 2372  
 gtggcacctg gccaccaact gtcaactgcg gggccatgtg ctctgtgca cacaagctgg 2432  
 ctctacacat tcaaggggca ctgctctggg tcttactccc tgteccaccc cagctctcct 2492  
 agaaccagac cggcaccatg gggctccacc acacacctct gtccacctcc ataattcctg 2552  
 agactgctag cagctctctg tcaagtcacc accgtccccc ctgagccccc cgggccactg 2612  
 ttcaaaaagaa taggcaccaa ctacccttct gctctctgcc acctgtgtga cgtgaccact 2672  
 ccagctccct gagcgtgaaa actgctggct acgtgctgct gtccctcctg tgtgggacca 2732  
 gtctgttccg gggagacggt tgagtccagc agcacatcca ctgaagcagc tgatctgact 2792  
 gaaggacttg agggcatgag aatccccgc tggcccttcc attgcctcag agctggcctc 2852  
 cctgagggggg tgtcaactgg agtgtctact gtgaagctct tacatagtgg caccctgata 2912  
 tctcctgggg ttcccttgtg ttggggtgag gaggcagagg tcaaggtcag agtgccccta 2972  
 gaaggctctc cagagatgtg aactcaggtc cccagacaca agcctggggt caaagggcag 3032  
 ggcaagtctt ggtccacgtt catggtgctg acccaggccc tctgagaagg ccctgtcatt 3092  
 cctattctga tgtcctgagg acgcccattt gtaggttttt ggttttaaat caagccacag 3152  
 ccacagtcat ttggcccaat gctttgcatt gtgttgcct aacacatcac tgccctgtgg 3212  
 aacccccctg cctggccctt ttcagtggtc agtgtccagt gctgggtacg gtgtgttccc 3272

accacactgg gtccacctgc tgtgccactg gacttagtgc tgtggttgta atgtctttta 3332  
ctattgtatt aatgactagt ctgttacatt agactggggg tggggtgcaa gggctctgctg 3392  
gtttgtgagg ctttttgatt ggggggggtgg tttgtttttt ttttttaaag ctattggagt 3452  
tct 3455

<210> 4  
<211> 512  
<212> PRT  
<213> Rat

<400> 4

Met	Ala	Val	Ala	Gly	Ala	Lys	Arg	Arg	Ala	Val	Ala	Ala	Pro	Ala	Thr	1	5	10	15
Thr	Ala	Ala	Glu	Glu	Glu	Arg	Gln	Ala	Arg	Glu	Lys	Met	Leu	Glu	Ala	20	25	30	
Arg	Arg	Gly	Asp	Gly	Ala	Asp	Pro	Glu	Gly	Glu	Gly	Val	Thr	Leu	Gln	35	40	45	
Arg	Asn	Ile	Thr	Leu	Ile	Asn	Gly	Val	Ala	Ile	Ile	Val	Gly	Thr	Ile	50	55	60	
Ile	Gly	Ser	Gly	Ile	Phe	Val	Thr	Pro	Thr	Gly	Val	Leu	Lys	Glu	Ala	65	70	75	80
Gly	Ser	Pro	Gly	Leu	Ser	Leu	Val	Val	Trp	Ala	Val	Cys	Gly	Val	Phe	85	90	95	
Ser	Ile	Val	Gly	Ala	Leu	Cys	Tyr	Ala	Glu	Leu	Gly	Thr	Thr	Ile	Ser	100	105	110	
Lys	Ser	Gly	Gly	Asp	Tyr	Ala	Tyr	Met	Leu	Glu	Val	Tyr	Gly	Ser	Leu	115	120	125	
Pro	Ala	Phe	Leu	Lys	Leu	Trp	Ile	Glu	Leu	Leu	Ile	Ile	Arg	Pro	Ser	130	135	140	
Ser	Gln	Tyr	Ile	Val	Ala	Leu	Val	Phe	Ala	Thr	Tyr	Leu	Leu	Lys	Pro	145	150	155	160
Val	Phe	Pro	Thr	Cys	Pro	Val	Pro	Glu	Glu	Ala	Ala	Lys	Leu	Val	Ala	165	170	175	
Cys	Leu	Cys	Val	Leu	Leu	Leu	Thr	Ala	Val	Asn	Cys	Tyr	Ser	Val	Lys	180	185	190	
Ala	Ala	Thr	Arg	Val	Gln	Asp	Ala	Phe	Ala	Ala	Ala	Lys	Leu	Leu	Ala	195	200	205	
Leu	Ala	Leu	Ile	Ile	Leu	Leu	Gly	Phe	Ile	Gln	Met	Gly	Lys	Asp	Ile	210	215	220	

Gly	Gln	Gly	Asp	Ala	Ser	Asn	Leu	His	Gln	Lys	Leu	Ser	Phe	Glu	Gly	225	230	235	240
Thr	Asn	Leu	Asp	Val	Gly	Asn	Ile	Val	Leu	Ala	Leu	Tyr	Ser	Gly	Leu	245	250	255	
Phe	Ala	Tyr	Gly	Gly	Trp	Asn	Tyr	Leu	Asn	Phe	Val	Thr	Glu	Glu	Met	260	265	270	
Ile	Asn	Pro	Tyr	Arg	Asn	Leu	Pro	Leu	Ala	Ile	Ile	Ile	Ser	Leu	Pro	275	280	285	
Ile	Val	Thr	Leu	Val	Tyr	Val	Leu	Thr	Asn	Leu	Ala	Tyr	Phe	Thr	Thr	290	295	300	
Leu	Ser	Thr	Asn	Gln	Met	Leu	Thr	Ser	Glu	Ala	Val	Ala	Val	Asp	Phe	305	310	315	320
Gly	Asn	Tyr	His	Leu	Gly	Val	Met	Ser	Trp	Ile	Ile	Pro	Val	Phe	Val	325	330	335	
Gly	Leu	Ser	Cys	Phe	Gly	Ser	Val	Asn	Gly	Ser	Leu	Phe	Thr	Ser	Ser	340	345	350	
Arg	Leu	Phe	Phe	Val	Gly	Ser	Arg	Glu	Gly	His	Leu	Pro	Ser	Ile	Leu	355	360	365	
Ser	Met	Ile	His	Pro	Gln	Leu	Leu	Thr	Pro	Val	Pro	Ser	Leu	Val	Phe	370	375	380	
Thr	Cys	Val	Met	Thr	Leu	Met	Tyr	Ala	Phe	Ser	Arg	Asp	Ile	Phe	Ser	385	390	395	400
Ile	Ile	Asn	Phe	Phe	Ser	Phe	Phe	Asn	Trp	Leu	Cys	Val	Ala	Leu	Ala	405	410	415	
Ile	Ile	Gly	Met	Met	Trp	Leu	Arg	Phe	Lys	Lys	Pro	Glu	Leu	Glu	Arg	420	425	430	
Pro	Ile	Lys	Val	Asn	Leu	Ala	Leu	Pro	Val	Phe	Phe	Ile	Leu	Ala	Cys	435	440	445	
Leu	Phe	Leu	Ile	Ala	Val	Ser	Phe	Trp	Lys	Thr	Pro	Leu	Glu	Cys	Gly	450	455	460	
Ile	Gly	Phe	Ala	Ile	Ile	Leu	Ser	Gly	Leu	Pro	Val	Tyr	Phe	Phe	Gly	465	470	475	480
Val	Trp	Trp	Lys	Asn	Lys	Pro	Lys	Trp	Ile	Leu	Gln	Val	Ile	Phe	Ser	485	490	495	
Val	Thr	Val	Leu	Cys	Gln	Lys	Leu	Met	Gln	Val	Val	Pro	Gln	Glu	Thr	500	505	510	

<210> 5

<211> 1863

<212> DNA  
<213> Homo sapiens

<220>  
<221> 5'UTR  
<222> (1)..(109)

<220>  
<221> CDS  
<222> (110)..(1699)

<220>  
<221> 3'UTR  
<222> (1700)..(1863)

<400> 5  
gcgcggagcc acagaggccg gggagagcgt tctgggtccg aggtccagg taggggttga 60  
  
gccaccatct gaccgcaagc tgcgtcgtgt cgccggttct gcaggcacc atg agc cag 118  
Met Ser Gln  
1

gac acc gag gtg gat atg aag gag gtg gag ctg aat gag tta gag ccc 166  
Asp Thr Glu Val Asp Met Lys Glu Val Glu Leu Asn Glu Leu Glu Pro  
5 10 15

gag aag cag ccg atg aac gcg gcg tct ggg gcg gcc atg tcc ctg gcg 214  
Glu Lys Gln Pro Met Asn Ala Ala Ser Gly Ala Ala Met Ser Leu Ala  
20 25 30 35

gga gcc gag aag aat ggt ctg gtg aag atc aag gtg gcg gaa gac gag 262  
Gly Ala Glu Lys Asn Gly Leu Val Lys Ile Lys Val Ala Glu Asp Glu  
40 45 50

gcg gag gcg gca gcc gcg gct aag ttc acg ggc ctg tcc aag gag gag 310  
Ala Glu Ala Ala Ala Ala Lys Phe Thr Gly Leu Ser Lys Glu Glu  
55 60 65

ctg ctg aag gtg gca ggc agc ccc ggc tgg gta cgc acc cgc tgg gca 358  
Leu Leu Lys Val Ala Gly Ser Pro Gly Trp Val Arg Thr Arg Trp Ala  
70 75 80

ctg ctg ctg ctc ttc tgg ctc ggc tgg ctc ggc atg ctt gct ggt gcc 406  
Leu Leu Leu Leu Phe Trp Leu Gly Trp Leu Gly Met Leu Ala Gly Ala  
85 90 95

gtg gtc ata atc gtg cga gcg ccg cgt tgt cgc gag cta ccg gcg cag 454  
Val Val Ile Ile Val Arg Ala Pro Arg Cys Arg Glu Leu Pro Ala Gln  
100 105 110 115

aag tgg tgg cac acg ggc gcc ctc tac cgc atc ggc gac ctt cag gcc 502  
Lys Trp Trp His Thr Gly Ala Leu Tyr Arg Ile Gly Asp Leu Gln Ala  
120 125 130

ttc cag ggc cac ggc gcg ggc aac ctg gcg ggt ctg aag ggg cgt ctc 550  
Phe Gln Gly His Gly Ala Gly Asn Leu Ala Gly Leu Lys Gly Arg Leu  
135 140 145

gat tac ctg agc tct ctg aag gtg aag ggc ctt gtg ctg ggt cca att	598
Asp Tyr Leu Ser Ser Leu Lys Val Lys Gly Leu Val Leu Gly Pro Ile	
150 155 160	
cac aag aac cag aag gat gat gtc gct cag act gac ttg ctg cag atc	646
His Lys Asn Gln Lys Asp Asp Val Ala Gln Thr Asp Leu Leu Gln Ile	
165 170 175	
gac ccc aat ttt ggc tcc aag gaa gat ttt gac agt ctc ttg caa tcg	694
Asp Pro Asn Phe Gly Ser Lys Glu Asp Phe Asp Ser Leu Leu Gln Ser	
180 185 190 195	
gct aaa aaa aag agc atc cgt gtc att ctg gac ctt act ccc aac tac	742
Ala Lys Lys Lys Ser Ile Arg Val Ile Leu Asp Leu Thr Pro Asn Tyr	
200 205 210	
cgg ggt gag aac tcg tgg ttc tcc act cag gtt gac act gtg gcc acc	790
Arg Gly Glu Asn Ser Trp Phe Ser Thr Gln Val Asp Thr Val Ala Thr	
215 220 225	
aag gtg aag gat gct ctg gag ttt tgg ctg caa gct ggc gtg gat ggg	838
Lys Val Lys Asp Ala Leu Glu Phe Trp Leu Gln Ala Gly Val Asp Gly	
230 235 240	
ttc cag gtt cgg gac ata gag aat ctg aag gat gca tcc tca ttc ttg	886
Phe Gln Val Arg Asp Ile Glu Asn Leu Lys Asp Ala Ser Ser Phe Leu	
245 250 255	
gct gag tgg caa aat atc acc aag ggc ttc agt gaa gac agg ctc ttg	934
Ala Glu Trp Gln Asn Ile Thr Lys Gly Phe Ser Glu Asp Arg Leu Leu	
260 265 270 275	
att gcg ggg act aac tcc tcc gac ctt cag cag atc ctg agc cta ctc	982
Ile Ala Gly Thr Asn Ser Ser Asp Leu Gln Gln Ile Leu Ser Leu Leu	
280 285 290	
gaa tcc aac aaa gac ttg ctg ttg act agc tca tac ctg tct gat tct	1030
Glu Ser Asn Lys Asp Leu Leu Leu Thr Ser Ser Tyr Leu Ser Asp Ser	
295 300 305	
ggg tct act ggg gag cat aca aaa tcc cta gtc aca cag tat ttg aat	1078
Gly Ser Thr Gly Glu His Thr Lys Ser Leu Val Thr Gln Tyr Leu Asn	
310 315 320	
gcc act ggc aat cgc tgg tgc agc tgg agt ttg tct cag gca agg ctc	1126
Ala Thr Gly Asn Arg Trp Cys Ser Trp Ser Leu Ser Gln Ala Arg Leu	
325 330 335	
ctg act tcc ttc ttg ccg gct caa ctt ctc cga ctc tac cag ctg atg	1174
Leu Thr Ser Phe Leu Pro Ala Gln Leu Leu Arg Leu Tyr Gln Leu Met	
340 345 350 355	
ctc ttc acc ctg cca ggg acc cct gtt ttc agc tac ggg gat gag att	1222
Leu Phe Thr Leu Pro Gly Thr Pro Val Phe Ser Tyr Gly Asp Glu Ile	
360 365 370	

ggc ctg gat gca gct gcc ctt cct gga cag cct atg gag gct cca gtc 1270  
 Gly Leu Asp Ala Ala Ala Leu Pro Gly Gln Pro Met Glu Ala Pro Val  
                   375                  380                  385

atg ctg tgg gat gag tcc agc ttc cct gac atc cca ggg gct gta agt 1318  
 Met Leu Trp Asp Glu Ser Ser Phe Pro Asp Ile Pro Gly Ala Val Ser  
                   390                  395                  400

gcc aac atg act gtg aag ggc cag agt gaa gac cct ggc tcc ctc ctt 1366  
 Ala Asn Met Thr Val Lys Gly Gln Ser Glu Asp Pro Gly Ser Leu Leu  
                   405                  410                  415

tcc ttg ttc cgg cgg ctg agt gac cag cgg agt aag gag cgc tcc cta 1414  
 Ser Leu Phe Arg Arg Leu Ser Asp Gln Arg Ser Lys Glu Arg Ser Leu  
 420                  425                  430                  435

ctg cat ggg gac ttc cac gcg ttc tcc gct ggg cct gga ctc ttc tcc 1462  
 Leu His Gly Asp Phe His Ala Phe Ser Ala Gly Pro Gly Leu Phe Ser  
                   440                  445                  450

tat atc cgc cac tgg gac cag aat gag cgt ttt ctg gta gtg ctt aac 1510  
 Tyr Ile Arg His Trp Asp Gln Asn Glu Arg Phe Leu Val Val Leu Asn  
                   455                  460                  465

ttt ggg gat gtg ggc ctc tcg gct gga ctg cag gcc tcc gac ctg cct 1558  
 Phe Gly Asp Val Gly Leu Ser Ala Gly Leu Gln Ala Ser Asp Leu Pro  
                   470                  475                  480

gcc agc gcc agc ctc cca gcc aag gct gac ctc ctg ctc agc acc cag 1606  
 Ala Ser Ala Ser Leu Pro Ala Lys Ala Asp Leu Leu Leu Ser Thr Gln  
                   485                  490                  495

cca ggc cgt gag gag ggc tcc cct ctt gag ctg gaa cgc ctg aaa ctg 1654  
 Pro Gly Arg Glu Glu Gly Ser Pro Leu Glu Leu Glu Arg Leu Lys Leu  
 500                  505                  510                  515

gag cct cac gaa ggg ctg ctg ctc cgc ttc ccc tac gcg gcc tga 1699  
 Glu Pro His Glu Gly Leu Leu Leu Arg Phe Pro Tyr Ala Ala  
                   520                  525                  530

cttcagcctg acatggaccc actacccttc tcctttcctt cccaggccct ttggttctga 1759

tttttctctt ttttaaaaac aaacaaacaa actgttgacg attatgagtg aacccccaaa 1819

@  
 taggggtgttt tctgccttca aataaaaagtc acccctgcat ggtg 1863

<210> 6  
 <211> 529  
 <212> PRT  
 <213> Homo sapiens

<400> 6  
 Met Ser Gln Asp Thr Glu Val Asp Met Lys Glu Val Glu Leu Asn Glu  
   1                  5                  10                  15

Leu Glu Pro Glu Lys Gln Pro Met Asn Ala Ala Ser Gly Ala Ala Met

20					25					30					
Ser	Leu	Ala	Gly	Ala	Glu	Lys	Asn	Gly	Leu	Val	Lys	Ile	Lys	Val	Ala
		35					40					45			
Glu	Asp	Glu	Ala	Glu	Ala	Ala	Ala	Ala	Ala	Lys	Phe	Thr	Gly	Leu	Ser
	50					55					60				
Lys	Glu	Glu	Leu	Leu	Lys	Val	Ala	Gly	Ser	Pro	Gly	Trp	Val	Arg	Thr
65					70					75					80
Arg	Trp	Ala	Leu	Leu	Leu	Leu	Phe	Trp	Leu	Gly	Trp	Leu	Gly	Met	Leu
			85						90					95	
Ala	Gly	Ala	Val	Val	Ile	Ile	Val	Arg	Ala	Pro	Arg	Cys	Arg	Glu	Leu
			100					105					110		
Pro	Ala	Gln	Lys	Trp	Trp	His	Thr	Gly	Ala	Leu	Tyr	Arg	Ile	Gly	Asp
	115						120					125			
Leu	Gln	Ala	Phe	Gln	Gly	His	Gly	Ala	Gly	Asn	Leu	Ala	Gly	Leu	Lys
	130					135					140				
Gly	Arg	Leu	Asp	Tyr	Leu	Ser	Ser	Leu	Lys	Val	Lys	Gly	Leu	Val	Leu
145					150					155					160
Gly	Pro	Ile	His	Lys	Asn	Gln	Lys	Asp	Asp	Val	Ala	Gln	Thr	Asp	Leu
				165					170					175	
Leu	Gln	Ile	Asp	Pro	Asn	Phe	Gly	Ser	Lys	Glu	Asp	Phe	Asp	Ser	Leu
			180					185					190		
Leu	Gln	Ser	Ala	Lys	Lys	Lys	Ser	Ile	Arg	Val	Ile	Leu	Asp	Leu	Thr
	195						200					205			
Pro	Asn	Tyr	Arg	Gly	Glu	Asn	Ser	Trp	Phe	Ser	Thr	Gln	Val	Asp	Thr
	210					215					220				
Val	Ala	Thr	Lys	Val	Lys	Asp	Ala	Leu	Glu	Phe	Trp	Leu	Gln	Ala	Gly
225					230					235					240
Val	Asp	Gly	Phe	Gln	Val	Arg	Asp	Ile	Glu	Asn	Leu	Lys	Asp	Ala	Ser
				245					250					255	
Ser	Phe	Leu	Ala	Glu	Trp	Gln	Asn	Ile	Thr	Lys	Gly	Phe	Ser	Glu	Asp
		260						265					270		
Arg	Leu	Leu	Ile	Ala	Gly	Thr	Asn	Ser	Ser	Asp	Leu	Gln	Gln	Ile	Leu
	275						280					285			
Ser	Leu	Leu	Glu	Ser	Asn	Lys	Asp	Leu	Leu	Leu	Thr	Ser	Ser	Tyr	Leu
	290					295					300				
Ser	Asp	Ser	Gly	Ser	Thr	Gly	Glu	His	Thr	Lys	Ser	Leu	Val	Thr	Gln
305					310					315					320
Tyr	Leu	Asn	Ala	Thr	Gly	Asn	Arg	Trp	Cys	Ser	Trp	Ser	Leu	Ser	Gln



325										330					335				
Ala	Arg	Leu	Leu	Thr	Ser	Phe	Leu	Pro	Ala	Gln	Leu	Leu	Arg	Leu	Tyr				
			340					345					350						
Gln	Leu	Met	Leu	Phe	Thr	Leu	Pro	Gly	Thr	Pro	Val	Phe	Ser	Tyr	Gly				
		355					360					365							
Asp	Glu	Ile	Gly	Leu	Asp	Ala	Ala	Ala	Leu	Pro	Gly	Gln	Pro	Met	Glu				
	370					375					380								
Ala	Pro	Val	Met	Leu	Trp	Asp	Glu	Ser	Ser	Phe	Pro	Asp	Ile	Pro	Gly				
385					390					395					400				
Ala	Val	Ser	Ala	Asn	Met	Thr	Val	Lys	Gly	Gln	Ser	Glu	Asp	Pro	Gly				
				405					410					415					
Ser	Leu	Leu	Ser	Leu	Phe	Arg	Arg	Leu	Ser	Asp	Gln	Arg	Ser	Lys	Glu				
			420					425					430						
Arg	Ser	Leu	Leu	His	Gly	Asp	Phe	His	Ala	Phe	Ser	Ala	Gly	Pro	Gly				
		435					440					445							
Leu	Phe	Ser	Tyr	Ile	Arg	His	Trp	Asp	Gln	Asn	Glu	Arg	Phe	Leu	Val				
	450					455					460								
Val	Leu	Asn	Phe	Gly	Asp	Val	Gly	Leu	Ser	Ala	Gly	Leu	Gln	Ala	Ser				
465					470					475					480				
Asp	Leu	Pro	Ala	Ser	Ala	Ser	Leu	Pro	Ala	Lys	Ala	Asp	Leu	Leu	Leu				
				485					490					495					
Ser	Thr	Gln	Pro	Gly	Arg	Glu	Glu	Gly	Ser	Pro	Leu	Glu	Leu	Glu	Arg				
			500					505					510						
Leu	Lys	Leu	Glu	Pro	His	Glu	Gly	Leu	Leu	Leu	Arg	Phe	Pro	Tyr	Ala				
		515					520					525							

Ala

<210> 7

<211> 1797

<212> DNA

<213> Rat

<220>

<221> 5'UTR

<222> (1)..(19)

<220>

<221> CDS

<222> (20)..(1603)

<220>

<221> 3'UTR

<222> (1604)..(1797)

<400> 7

cgttgctgtc gcaggtacc atg agc cag gac acc gaa gtg gac atg aaa gat	52
Met Ser Gln Asp Thr Glu Val Asp Met Lys Asp	
1 5 10	
gtg gag ctg aac gag ctg gaa ccg gag aag cag cct atg aat gca gcg	100
Val Glu Leu Asn Glu Leu Glu Pro Glu Lys Gln Pro Met Asn Ala Ala	
15 20 25	
gac ggg gcg gca gcc ggg gag aag aac ggt ctg gtg aag att aag gtg	148
Asp Gly Ala Ala Ala Gly Glu Lys Asn Gly Leu Val Lys Ile Lys Val	
30 35 40	
gcc gaa gac gag gcg gaa gcc ggg gtc aag ttc aca ggc tta tcc aag	196
Ala Glu Asp Glu Ala Glu Ala Gly Val Lys Phe Thr Gly Leu Ser Lys	
45 50 55	
gag gag cta ttg aag gta gct ggc agc ccg ggc tgg gtg cgc acc cgc	244
Glu Glu Leu Leu Lys Val Ala Gly Ser Pro Gly Trp Val Arg Thr Arg	
60 65 70 75	
tgg gcg ctg ctg ctg ctc ttc tgg ctc ggt tgg ctg ggt atg ctg gcg	292
Trp Ala Leu Leu Leu Leu Phe Trp Leu Gly Trp Leu Gly Met Leu Ala	
80 85 90	
ggc gcc gtg gtt atc atc gtt ccg gcg cca cgc tgc cgt gag ctg ccg	340
Gly Ala Val Val Ile Ile Val Arg Ala Pro Arg Cys Arg Glu Leu Pro	
95 100 105	
gta cag aga tgg tgg cac aag ggc gcc ctc tac cgc atc ggc gac ctt	388
Val Gln Arg Trp Trp His Lys Gly Ala Leu Tyr Arg Ile Gly Asp Leu	
110 115 120	
cag gcc ttc gta ggc ccg gaa gcg aga ggc ata gct ggt ctg aag aac	436
Gln Ala Phe Val Gly Pro Glu Ala Arg Gly Ile Ala Gly Leu Lys Asn	
125 130 135	
cat ctg gag tac ttg agc acc ctg aag gtg aag ggc cta gtt ttg ggc	484
His Leu Glu Tyr Leu Ser Thr Leu Lys Val Lys Gly Leu Val Leu Gly	
140 145 150 155	
cca att cac aag aac cag aag gat gaa gtc aat gaa acc gac ttg aaa	532
Pro Ile His Lys Asn Gln Lys Asp Glu Val Asn Glu Thr Asp Leu Lys	
160 165 170	
cag att gat ccc gat tta ggc tcc cag gaa gat ttt aaa gac ctt cta	580
Gln Ile Asp Pro Asp Leu Gly Ser Gln Glu Asp Phe Lys Asp Leu Leu	
175 180 185	
caa agt gcc aag aaa aag agc att cac atc att ttg gac ctc act ccc	628
Gln Ser Ala Lys Lys Lys Ser Ile His Ile Ile Leu Asp Leu Thr Pro	
190 195 200	
aac tat aag ggc cag aat gca tgg ttc ctc cct cct cag gct gac att	676
Asn Tyr Lys Gly Gln Asn Ala Trp Phe Leu Pro Pro Gln Ala Asp Ile	
205 210 215	

gta gcc acc aaa atg aag gag gct ctg agt tct tgg ttg cag gac ggt	724
Val Ala Thr Lys Met Lys Glu Ala Leu Ser Ser Trp Leu Gln Asp Gly	
220 225 230 235	
gtg gat ggg ttc caa gtt cgg gat gtg gga aag ctg gcg aat gca tcc	772
Val Asp Gly Phe Gln Val Arg Asp Val Gly Lys Leu Ala Asn Ala Ser	
240 245 250	
ttg tac ttg gct gag tgg cag aat atc acc aag aac ttc agt gag gac	820
Leu Tyr Leu Ala Glu Trp Gln Asn Ile Thr Lys Asn Phe Ser Glu Asp	
255 260 265	
agg ctt ttg att gca ggg acc gcg tcc tct gac ctg caa caa att gtc	868
Arg Leu Leu Ile Ala Gly Thr Ala Ser Ser Asp Leu Gln Gln Ile Val	
270 275 280	
aac ata ctt gaa tcc acc agc gat ctg ctg ctg acc agc tca tac ctg	916
Asn Ile Leu Glu Ser Thr Ser Asp Leu Leu Leu Thr Ser Ser Tyr Leu	
285 290 295	
tca cag ccc gtt ttc act ggg gag cat gca gaa ctc cta gtg att aag	964
Ser Gln Pro Val Phe Thr Gly Glu His Ala Glu Leu Leu Val Ile Lys	
300 305 310 315	
tat ttg aat gcc act ggc agc cgc tgg tgc agc tgg agt gtg tcg cag	1012
Tyr Leu Asn Ala Thr Gly Ser Arg Trp Cys Ser Trp Ser Val Ser Gln	
320 325 330	
gca gga ctc ctg aca tcc ttt ata ccg gct cag ttt ctc cga ctc tac	1060
Ala Gly Leu Leu Thr Ser Phe Ile Pro Ala Gln Phe Leu Arg Leu Tyr	
335 340 345	
cag ctg ctg ctc ttc act ctg cca gga act cct gtt ttc agc tat ggg	1108
Gln Leu Leu Leu Phe Thr Leu Pro Gly Thr Pro Val Phe Ser Tyr Gly	
350 355 360	
gat gag ctt ggc ctt cag gca gtt gcc ctt cct gga cag cct atg gag	1156
Asp Glu Leu Gly Leu Gln Ala Val Ala Leu Pro Gly Gln Pro Met Glu	
365 370 375	
gct cca ttc atg ctg tgg aat gag tct agc aac tcc caa acc tca agt	1204
Ala Pro Phe Met Leu Trp Asn Glu Ser Ser Asn Ser Gln Thr Ser Ser	
380 385 390 395	
cct gta agc ctc aac atg aca gtg aag ggc caa aat gaa gac ccc ggc	1252
Pro Val Ser Leu Asn Met Thr Val Lys Gly Gln Asn Glu Asp Pro Gly	
400 405 410	
tcc ctc ctc acc cag ttc cgg cga ctg agt gac ctc cgt ggt aag gag	1300
Ser Leu Leu Thr Gln Phe Arg Arg Leu Ser Asp Leu Arg Gly Lys Glu	
415 420 425	
cgc tct ctg tta cac ggt gac ttt gat gca ctg tct tcc tca tct ggg	1348
Arg Ser Leu Leu His Gly Asp Phe Asp Ala Leu Ser Ser Ser Ser Gly	
430 435 440	

ctc ttc tcc tac gtc cgc cac tgg gac cag aat gag cgt tac ctg gtg 1396  
 Leu Phe Ser Tyr Val Arg His Trp Asp Gln Asn Glu Arg Tyr Leu Val  
 445 450 455

gtg ctc aac ttc cag gat gtg ggc ctg tca gcc agg gta gga gcc tcc 1444  
 Val Leu Asn Phe Gln Asp Val Gly Leu Ser Ala Arg Val Gly Ala Ser  
 460 465 470 475

aac ctc cct gct ggc ata agc ctg cca gcc agt gct aac ctt ttg ctt 1492  
 Asn Leu Pro Ala Gly Ile Ser Leu Pro Ala Ser Ala Asn Leu Leu Leu  
 480 485 490

agt act gac agc acc cgg cta agc cgt gag gag ggc acc tcc ctg agc 1540  
 Ser Thr Asp Ser Thr Arg Leu Ser Arg Glu Glu Gly Thr Ser Leu Ser  
 495 500 505

ctg gaa aac ctg agc ctg aat cct tat gag ggc ttg ttg tta cag ttc 1588  
 Leu Glu Asn Leu Ser Leu Asn Pro Tyr Glu Gly Leu Leu Leu Gln Phe  
 510 515 520

cct ttt gtg gcc tga tccctctaca cagaacctgc cacccttctt tcctctctca 1643  
 Pro Phe Val Ala  
 525

ggcctttgga attctgggtct ttctctcctt attttgtttt tgttttttaaa cttttgcaga 1703

ttacatatga attcttacac tggggggtttt tgtttttcaaa ataaaaaaaa tcacccttaa 1763

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1797

<210> 8  
 <211> 527  
 <212> PRT  
 <213> Rat

<400> 8  
 Met Ser Gln Asp Thr Glu Val Asp Met Lys Asp Val Glu Leu Asn Glu  
 1 5 10 15  
 Leu Glu Pro Glu Lys Gln Pro Met Asn Ala Ala Asp Gly Ala Ala Ala  
 20 25 30  
 Gly Glu Lys Asn Gly Leu Val Lys Ile Lys Val Ala Glu Asp Glu Ala  
 35 40 45  
 Glu Ala Gly Val Lys Phe Thr Gly Leu Ser Lys Glu Glu Leu Leu Lys  
 50 55 60  
 Val Ala Gly Ser Pro Gly Trp Val Arg Thr Arg Trp Ala Leu Leu Leu  
 65 70 75 80  
 Leu Phe Trp Leu Gly Trp Leu Gly Met Leu Ala Gly Ala Val Val Ile  
 85 90 95  
 Ile Val Arg Ala Pro Arg Cys Arg Glu Leu Pro Val Gln Arg Trp Trp  
 100 105 110

His	Lys	Gly	Ala	Leu	Tyr	Arg	Ile	Gly	Asp	Leu	Gln	Ala	Phe	Val	Gly
		115					120					125			
Pro	Glu	Ala	Arg	Gly	Ile	Ala	Gly	Leu	Lys	Asn	His	Leu	Glu	Tyr	Leu
	130					135					140				
Ser	Thr	Leu	Lys	Val	Lys	Gly	Leu	Val	Leu	Gly	Pro	Ile	His	Lys	Asn
145					150					155					160
Gln	Lys	Asp	Glu	Val	Asn	Glu	Thr	Asp	Leu	Lys	Gln	Ile	Asp	Pro	Asp
				165					170					175	
Leu	Gly	Ser	Gln	Glu	Asp	Phe	Lys	Asp	Leu	Leu	Gln	Ser	Ala	Lys	Lys
			180					185					190		
Lys	Ser	Ile	His	Ile	Ile	Leu	Asp	Leu	Thr	Pro	Asn	Tyr	Lys	Gly	Gln
		195					200					205			
Asn	Ala	Trp	Phe	Leu	Pro	Pro	Gln	Ala	Asp	Ile	Val	Ala	Thr	Lys	Met
		210				215					220				
Lys	Glu	Ala	Leu	Ser	Ser	Trp	Leu	Gln	Asp	Gly	Val	Asp	Gly	Phe	Gln
225					230					235					240
Val	Arg	Asp	Val	Gly	Lys	Leu	Ala	Asn	Ala	Ser	Leu	Tyr	Leu	Ala	Glu
				245					250					255	
Trp	Gln	Asn	Ile	Thr	Lys	Asn	Phe	Ser	Glu	Asp	Arg	Leu	Leu	Ile	Ala
			260					265					270		
Gly	Thr	Ala	Ser	Ser	Asp	Leu	Gln	Gln	Ile	Val	Asn	Ile	Leu	Glu	Ser
		275					280					285			
Thr	Ser	Asp	Leu	Leu	Leu	Thr	Ser	Ser	Tyr	Leu	Ser	Gln	Pro	Val	Phe
		290				295					300				
Thr	Gly	Glu	His	Ala	Glu	Leu	Leu	Val	Ile	Lys	Tyr	Leu	Asn	Ala	Thr
305					310					315					320
Gly	Ser	Arg	Trp	Cys	Ser	Trp	Ser	Val	Ser	Gln	Ala	Gly	Leu	Leu	Thr
				325					330					335	
Ser	Phe	Ile	Pro	Ala	Gln	Phe	Leu	Arg	Leu	Tyr	Gln	Leu	Leu	Leu	Phe
			340					345					350		
Thr	Leu	Pro	Gly	Thr	Pro	Val	Phe	Ser	Tyr	Gly	Asp	Glu	Leu	Gly	Leu
		355					360					365			
Gln	Ala	Val	Ala	Leu	Pro	Gly	Gln	Pro	Met	Glu	Ala	Pro	Phe	Met	Leu
						375					380				
Trp	Asn	Glu	Ser	Ser	Asn	Ser	Gln	Thr	Ser	Ser	Pro	Val	Ser	Leu	Asn
385					390					395					400
Met	Thr	Val	Lys	Gly	Gln	Asn	Glu	Asp	Pro	Gly	Ser	Leu	Leu	Thr	Gln
				405					410					415	

Phe Arg Arg Leu Ser Asp Leu Arg Gly Lys Glu Arg Ser Leu Leu His  
                   420                                  425                                  430  
 Gly Asp Phe Asp Ala Leu Ser Ser Ser Ser Gly Leu Phe Ser Tyr Val  
                   435                                  440                                  445  
 Arg His Trp Asp Gln Asn Glu Arg Tyr Leu Val Val Leu Asn Phe Gln  
                   450                                  455                                  460  
 Asp Val Gly Leu Ser Ala Arg Val Gly Ala Ser Asn Leu Pro Ala Gly  
                   465                                  470                                  475                                  480  
 Ile Ser Leu Pro Ala Ser Ala Asn Leu Leu Leu Ser Thr Asp Ser Thr  
                                   485                                  490                                  495  
 Arg Leu Ser Arg Glu Glu Gly Thr Ser Leu Ser Leu Glu Asn Leu Ser  
                                   500                                  505                                  510  
 Leu Asn Pro Tyr Glu Gly Leu Leu Leu Gln Phe Pro Phe Val Ala  
                   515                                  520                                  525

<210> 9  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Artificially  
           synthesized primer sequence

<220>  
 <221> primer\_bind  
 <222> (1)..(22)

<400> 9  
 cgaagtggac atgaaagatg tg

22

<210> 10  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Artificially  
           synthesized primer sequence

<220>  
 <221> primer\_bind  
 <222> (1)..(22)

<400> 10  
 aaactaggcc cttcaccttc ag

22

<210> 11  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Artificially  
synthesized primer sequence

<220>  
<221> primer\_bind  
<222> (1)..(24)

<400> 11  
actgctgctg ctcttctggc tcgg

24

<210> 12  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Artificially  
synthesized primer sequence

<220>  
<221> primer\_bind  
<222> (1)..(24)

<400> 12  
gtggatgggt tccaggttcg ggac

24

<210> 13  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Artificially  
synthesized primer sequence

<220>  
<221> primer\_bind  
<222> (1)..(24)

<400> 13  
tgctgtggga tgagtccagc ttcc

24

<210> 14  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
synthesized primer sequence

<220>

<221> primer\_bind

<222> (1)..(24)

<400> 14

gcaggagggtc agccttggct ggca

24

<210> 15

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
synthesized primer sequence

<220>

<221> primer\_bind

<222> (1)..(24)

<400> 15

cttgctgag acaaactcca gctg

24

<210> 16

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
synthesized primer sequence

<220>

<221> primer\_bind

<222> (1)..(24)

<400> 16

actgtcaaaa tcttccttgg agcc

24

<210> 17

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
synthesized primer sequence

<220>

<221> primer\_bind

<222> (1)..(24)



<400> 17  
ttctcgggct ctaactcatt cagc 24

<210> 18  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Artificially  
synthesized primer sequence

<220>  
<221> primer\_bind  
<222> (1)..(23)

<400> 18  
tgctgctgct cacggccgtg aac 23

<210> 19  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Artificially  
synthesized primer sequence

<220>  
<221> primer\_bind  
<222> (1)..(17)

<400> 19  
tggcggcctt cacgctg 17

<210> 20  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Artificially  
synthesized primer sequence

<220>  
<221> primer\_bind  
<222> (1)..(25)

<400> 20  
atctagattg gacacatcac ccttc 25

<210> 21

<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Artificially  
synthesized primer sequence

<220>  
<221> primer\_bind  
<222> (1)..(22)

<400> 21  
gtggtgaagt aggccagggt gg

22

<210> 22  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Artificially  
synthesized primer sequence

<220>  
<221> primer\_bind  
<222> (1)..(21)

<400> 22  
gtgggggtccc ggaaggcca c

21

<210> 23  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Artificially  
synthesized primer sequence

<220>  
<221> primer\_bind  
<222> (1)..(22)

<400> 23  
cttggttttc caccagacc cg

22

<210> 24  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Artificially

# synthesized primer sequence

<220>

<221> primer\_bind

<222> (1)..(22)

<400> 24

tgagggatga gattcgtacc ag

22

<210> 25

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially synthesized primer sequence

<220>

<221> primer\_bind

<222> (1)..(23)

<400> 25

cctgggagga atcaccacc ttg

23

<210> 26

<211> 1524

<212> RNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1524)

<400> 26

aug gcg ggu gcg ggc ccg aag cgg cgc gcg cua gcg gcg ccg gcg gcc	48
Met Ala Gly Ala Gly Pro Lys Arg Arg Ala Leu Ala Ala Pro Ala Ala	
1 5 10 15	

gag gag aag gaa gag gcg cgg gag aag aug cug gcc gcc aag agc gcg	96
Glu Glu Lys Glu Glu Ala Arg Glu Lys Met Leu Ala Ala Lys Ser Ala	
20 25 30	

gac ggc ucg gcg ccg gca ggc gag ggc gag ggc gug acc cug cag cgg	144
Asp Gly Ser Ala Pro Ala Gly Glu Gly Glu Gly Val Thr Leu Gln Arg	
35 40 45	

aac auc acg cug cuc aac ggc gug gcc auc auc gug ggg acc auu auc	192
Asn Ile Thr Leu Leu Asn Gly Val Ala Ile Ile Val Gly Thr Ile Ile	
50 55 60	

ggc ucg ggc auc uuc gug acg ccc acg ggc gug cuc aag gag gca ggc	240
Gly Ser Gly Ile Phe Val Thr Pro Thr Gly Val Leu Lys Glu Ala Gly	
65 70 75 80	

ucg ccg ggg cug gcg cug gug gug ugg gcc gcg ugc ggc guc uuc ucc	288
Ser Pro Gly Leu Ala Leu Val Val Trp Ala Ala Cys Gly Val Phe Ser	
85 90 95	
auc gug ggc gcg cuc ugc uac gcg gag cuc ggc acc acc auc ucc aaa	336
Ile Val Gly Ala Leu Cys Tyr Ala Glu Leu Gly Thr Thr Ile Ser Lys	
100 105 110	
ucg ggc ggc gac uac gcc uac aug cug gag guc uac ggc ugc cug ccc	384
Ser Gly Gly Asp Tyr Ala Tyr Met Leu Glu Val Tyr Gly Ser Leu Pro	
115 120 125	
gcc uuc cuc aag cuc ugg auc gag cug cuc auc auc cgg ccu uca ugc	432
Ala Phe Leu Lys Leu Trp Ile Glu Leu Leu Ile Ile Arg Pro Ser Ser	
130 135 140	
cag uac auc gug gcc cug guc uuc gcc acc uac cug cuc aag ccg cuc	480
Gln Tyr Ile Val Ala Leu Val Phe Ala Thr Tyr Leu Leu Lys Pro Leu	
145 150 155 160	
uuc ccc acc ugc ccg gug ccc gag gag gca gcc aag cuc gug gcc ugc	528
Phe Pro Thr Cys Pro Val Pro Glu Glu Ala Ala Lys Leu Val Ala Cys	
165 170 175	
cuc ugc gug cug cug cuc acg gcc gug aac ugc uac agc gug aag gcc	576
Leu Cys Val Leu Leu Leu Thr Ala Val Asn Cys Tyr Ser Val Lys Ala	
180 185 190	
gcc acc cgg guc cag gau gcc uuu gcc gcc gcc aag cuc cug gcc cug	624
Ala Thr Arg Val Gln Xaa Ala Phe Ala Ala Ala Lys Leu Leu Ala Leu	
195 200 205	
gcc cug auc auc cug cug ggc uuc guc cag auc ggg aag ggu gau gug	672
Ala Leu Ile Ile Leu Leu Gly Phe Val Gln Ile Gly Lys Gly Xaa Val	
210 215 220	
ucc aaU cua gau ccc aac uuc uca uuu gaa ggc acc aaa cug gau gug	720
Ser Asn Leu Xaa Pro Asn Phe Ser Phe Glu Gly Thr Lys Leu Xaa Val	
225 230 235 240	
ggg aac auu gug cug gca uua uac agc ggc cuc uuu gcc uau gga gga	768
Gly Asn Ile Val Leu Ala Leu Tyr Ser Gly Leu Phe Ala Tyr Gly Gly	
245 250 255	
ugg aaU uac uug aaU uuc guc aca gag gaa aug auc aac ccc uac aga	816
Trp Asn Tyr Leu Asn Phe Val Thr Glu Glu Met Ile Asn Pro Tyr Arg	
260 265 270	
aac cug ccc cug gcc auc auc auc ucc cug ccc auc gug acg cug gug	864
Asn Leu Pro Leu Ala Ile Ile Ile Ser Leu Pro Ile Val Thr Leu Val	
275 280 285	
uac gug cug acc aac cug gcc uac uuc acc acc cug ucc acc gag cag	912
Tyr Val Leu Thr Asn Leu Ala Tyr Phe Thr Thr Leu Ser Thr Glu Gln	
290 295 300	
aug cug ugc ucc gag gcc gug gcc gug gac uuc ggg aac uau cac cug	960

Met	Leu	Ser	Ser	Glu	Ala	Val	Ala	Val	Asp	Phe	Gly	Asn	Tyr	His	Leu	
305					310					315					320	
ggc	guc	aug	ucc	ugg	auc	auc	ccc	guc	uuc	gug	ggc	cug	ucc	ugc	uuc	1008
Gly	Val	Met	Ser	Trp	Ile	Ile	Pro	Val	Phe	Val	Gly	Leu	Ser	Cys	Phe	
				325					330					335		
ggc	ucc	guc	aaU	ggg	ucc	cug	uuc	aca	ucc	ucc	agg	cuc	uuc	uuc	gug	1056
Gly	Ser	Val	Asn	Gly	Ser	Leu	Phe	Thr	Ser	Ser	Arg	Leu	Phe	Phe	Val	
			340					345					350			
ggg	ucc	cgg	gaa	ggc	cac	cug	ccc	ucc	auc	cuc	ucc	aug	auc	cac	cca	1104
Gly	Ser	Arg	Glu	Gly	His	Leu	Pro	Ser	Ile	Leu	Ser	Met	Ile	His	Pro	
		355					360					365				
cag	cuc	cuc	acc	ccc	gug	ccg	ucc	cuc	gug	uuc	acg	ugu	gug	aug	acg	1152
Gln	Leu	Leu	Thr	Pro	Val	Pro	Ser	Leu	Val	Phe	Thr	Cys	Val	Met	Thr	
	370					375					380					
cug	cuc	uac	gcc	uuc	ucc	aag	gac	auc	uuc	ucc	guc	auc	aac	uuc	uuc	1200
Leu	Leu	Tyr	Ala	Phe	Ser	Lys	Asp	Ile	Phe	Ser	Val	Ile	Asn	Phe	Phe	
385					390					395					400	
agc	uuc	uuc	aac	ugg	cuc	ugc	gug	gcc	cug	gcc	auc	auc	ggc	aug	auc	1248
Ser	Phe	Phe	Asn	Trp	Leu	Cys	Val	Ala	Leu	Ala	Ile	Ile	Gly	Met	Ile	
			405					410					415			
ugg	cug	cgc	cac	aga	aag	ccu	gag	cuu	gag	cgg	ccc	auc	aag	gug	aac	1296
Trp	Leu	Arg	His	Arg	Lys	Pro	Glu	Leu	Glu	Arg	Pro	Ile	Lys	Val	Asn	
			420				425					430				
cug	gcc	cug	ccu	gug	uuc	uuc	auc	cug	gcc	ugc	cuc	uuc	cug	auc	gcc	1344
Leu	Ala	Leu	Pro	Val	Phe	Phe	Ile	Leu	Ala	Cys	Leu	Phe	Leu	Ile	Ala	
		435					440					445				
guc	ucc	uuc	ugg	aag	aca	ccc	gug	gag	ugu	ggc	auc	ggc	uuc	acc	auc	1392
Val	Ser	Phe	Trp	Lys	Thr	Pro	Val	Glu	Cys	Gly	Ile	Gly	Phe	Thr	Ile	
	450					455					460					
auc	cuc	agc	ggg	cug	ccc	guc	uac	uuc	uuc	ggg	guc	ugg	ugg	aaa	aac	1440
Ile	Leu	Ser	Gly	Leu	Pro	Val	Tyr	Phe	Phe	Gly	Val	Trp	Trp	Lys	Asn	
465					470					475					480	
aag	ccc	aag	ugg	cuc	cuc	cag	ggc	auc	uuc	ucc	acg	acc	guc	cug	ugu	1488
Lys	Pro	Lys	Trp	Leu	Leu	Gln	Gly	Ile	Phe	Ser	Thr	Thr	Val	Leu	Cys	
				485				490					495			
cag	aag	cuc	aug	cag	gug	guc	ccc	cag	gag	aca	uag					1524
Gln	Lys	Leu	Met	Gln	Val	Val	Pro	Gln	Glu	Thr						
			500					505								

<210> 27

<211> 1590

<212> RNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1590)

<400> 27

aug	agc	cag	gac	acc	gag	gug	gau	aug	aag	gag	gug	gag	cug	aa	gag	48
Met	Ser	Gln	Asp	Thr	Glu	Val	Xaa	Met	Lys	Glu	Val	Glu	Leu	Asn	Glu	
1				5					10					15		

uua	gag	ccc	gag	aag	cag	ccg	aug	aac	gcg	gcg	ucu	ggg	gcg	gcc	aug	96
Leu	Glu	Pro	Glu	Lys	Gln	Pro	Met	Asn	Ala	Ala	Ser	Gly	Ala	Ala	Met	
			20					25					30			

ucc	cug	gcg	gga	gcc	gag	aag	aa	ggu	cug	gug	aag	auc	aag	gug	gcg	144
Ser	Leu	Ala	Gly	Ala	Glu	Lys	Asn	Gly	Leu	Val	Lys	Ile	Lys	Val	Ala	
		35					40					45				

gaa	gac	gag	gcg	gag	gcg	gca	gcc	gcg	gcu	aag	uuc	acg	ggc	cug	ucc	192
Glu	Asp	Glu	Ala	Glu	Ala	Ala	Ala	Ala	Lys	Phe	Thr	Gly	Leu	Ser		
	50					55					60					

aag	gag	gag	cug	cug	aag	gug	gca	ggc	agc	ccc	ggc	ugg	gua	cgc	acc	240
Lys	Glu	Glu	Leu	Leu	Lys	Val	Ala	Gly	Ser	Pro	Gly	Trp	Val	Arg	Thr	
65					70				75						80	

cgc	ugg	gca	cug	cug	cug	cuc	uuc	ugg	cuc	ggc	ugg	cuc	ggc	aug	cuu	288
Arg	Trp	Ala	Leu	Leu	Leu	Leu	Phe	Trp	Leu	Gly	Trp	Leu	Gly	Met	Leu	
			85						90					95		

gcu	ggu	gcc	gug	guc	aua	auc	gug	cga	gcg	ccg	cgu	ugu	cgc	gag	cua	336
Ala	Gly	Ala	Val	Val	Ile	Ile	Val	Arg	Ala	Pro	Arg	Cys	Arg	Glu	Leu	
			100					105					110			

ccg	gcg	cag	aag	ugg	ugg	cac	acg	ggc	gcc	cuc	uac	cgc	auc	ggc	gac	384
Pro	Ala	Gln	Lys	Trp	Trp	His	Thr	Gly	Ala	Leu	Tyr	Arg	Ile	Gly	Asp	
		115					120					125				

cuu	cag	gcc	uuc	cag	ggc	cac	ggc	gcg	ggc	aac	cug	gcg	ggu	cug	aag	432
Leu	Gln	Ala	Phe	Gln	Gly	His	Gly	Ala	Gly	Asn	Leu	Ala	Gly	Leu	Lys	
	130					135					140					

ggg	cgu	cuc	gau	uac	cug	agc	ucu	cug	aag	gug	aag	ggc	cuu	gug	cug	480
Gly	Arg	Leu	Xaa	Tyr	Leu	Ser	Ser	Leu	Lys	Val	Lys	Gly	Leu	Val	Leu	
145					150					155					160	

ggu	cca	auu	cac	aag	aac	cag	aag	gau	gau	guc	gcu	cag	acu	gac	uug	528
Gly	Pro	Ile	His	Lys	Asn	Gln	Lys	Xaa	Xaa	Val	Ala	Gln	Xaa	Asp	Leu	
				165				170						175		

cug	cag	auc	gac	ccc	aa	uuu	ggc	ucc	aag	gaa	gau	uuu	gac	agu	cuc	576
Leu	Gln	Ile	Asp	Pro	Asn	Phe	Gly	Ser	Lys	Glu	Xaa	Phe	Asp	Ser	Leu	
			180					185					190			

uug	caa	ucg	gcu	aaa	aaa	aag	agc	auc	cgu	guc	auu	cug	gac	cuu	acu	624
Leu	Gln	Ser	Ala	Lys	Lys	Lys	Ser	Ile	Arg	Val	Ile	Leu	Asp	Leu	Xaa	
		195					200					205				

ccc aac uac cgg ggu gag aac ucg ugg uuc ucc acu cag guu gac acu	672
Pro Asn Tyr Arg Gly Glu Asn Ser Trp Phe Ser Xaa Gln Val Asp Xaa	
210 215 220	
gug gcc acc aag gug aag gau gcu cug gag uuu ugg cug caa gcu ggc	720
Val Ala Thr Lys Val Lys Xaa Ala Leu Glu Phe Trp Leu Gln Ala Gly	
225 230 235 240	
gug gau ggg uuc cag guu cgg gac aua gag aaU cug aag gau gca ucc	768
Val Xaa Gly Phe Gln Val Arg Asp Ile Glu Asn Leu Lys Xaa Ala Ser	
245 250 255	
uca uuc uug gcu gag ugg caa aaU auc acc aag ggc uuc agu gaa gac	816
Ser Phe Leu Ala Glu Trp Gln Asn Ile Thr Lys Gly Phe Ser Glu Asp	
260 265 270	
agg cuc uug auu gcg ggg acu aac ucc ucc gac cuu cag cag auc cug	864
Arg Leu Leu Ile Ala Gly Xaa Asn Ser Ser Asp Leu Gln Gln Ile Leu	
275 280 285	
agc cua cuc gaa ucc aac aaa gac uug cug uug acu agc uca uac cug	912
Ser Leu Leu Glu Ser Asn Lys Asp Leu Leu Leu Xaa Ser Ser Tyr Leu	
290 295 300	
ucu gau ucu ggu ucu acu ggg gag cau aca aaa ucc cua guc aca cag	960
Ser Xaa Ser Gly Ser Xaa Gly Glu His Thr Lys Ser Leu Val Thr Gln	
305 310 315 320	
uau uug aaU gcc acu ggc aaU cgc ugg ugc agc ugg agu uug ucu cag	1008
Tyr Leu Asn Ala Xaa Gly Asn Arg Trp Cys Ser Trp Ser Leu Ser Gln	
325 330 335	
gca agg cuc cug acu ucc uuc uug ccg gcu caa cuu cuc cga cuc uac	1056
Ala Arg Leu Leu Xaa Ser Phe Leu Pro Ala Gln Leu Leu Arg Leu Tyr	
340 345 350	
cag cug aug cuc uuc acc cug cca ggg acc ccu guu uuc agc uac ggg	1104
Gln Leu Met Leu Phe Thr Leu Pro Gly Thr Pro Val Phe Ser Tyr Gly	
355 360 365	
gau gag auu ggc cug gau gca gcu gcc cuu ccu gga cag ccu aug gag	1152
Xaa Glu Ile Gly Leu Xaa Ala Ala Ala Leu Pro Gly Gln Pro Met Glu	
370 375 380	
gcu cca guc aug cug ugg gau gag ucc agc uuc ccu gac auc cca ggg	1200
Ala Pro Val Met Leu Trp Xaa Glu Ser Ser Phe Pro Asp Ile Pro Gly	
385 390 395 400	
gcu gua agu gcc aac aug acu gug aag ggc cag agu gaa gac ccu ggc	1248
Ala Val Ser Ala Asn Met Xaa Val Lys Gly Gln Ser Glu Asp Pro Gly	
405 410 415	
ucc cuc cuu ucc uug uuc cgg cgg cug agu gac cag cgg agu aag gag	1296
Ser Leu Leu Ser Leu Phe Arg Arg Leu Ser Asp Gln Arg Ser Lys Glu	
420 425 430	
cgc ucc cua cug cau ggg gac uuc cac gcg uuc ucc gcu ggg ccu gga	1344

[illegible]